

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/564,369  
Source: IFWP  
Date Processed by STIC: 1-23-06

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 01/23/2006

PATENT APPLICATION: US/10/564,369

TIME: 09:55:55

Input Set : A:\sequence listing.txt

Output Set: N:\CRF4\01232006\J564369.raw

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3 <110> APPLICANT: Oregon Health & Science University
4   Moses, Ashlee
5   Nelson, Jay
6   Fruh, Klaus
7   King, Jeff
8   Jelinek, Laura
9   Hirsch, Alec
10  DeFilippis, Victor
12 <120> TITLE OF INVENTION: METHODS OF TREATMENT AND DIAGNOSIS USING
MODULATORS OF
13  VIRUS-INDUCED CELLULAR GENE SEQUENCES
15 <130> FILE REFERENCE: 899-73077-04
C--> 17 <140> CURRENT APPLICATION NUMBER: US/10/564,369
C--> 18 <141> CURRENT FILING DATE: 2006-01-11
20 <150> PRIOR APPLICATION NUMBER: PCT/US2004/011988
21 <151> PRIOR FILING DATE: 2004-04-15
23 <150> PRIOR APPLICATION NUMBER: US 60/486,694
24 <151> PRIOR FILING DATE: 2003-07-11
26 <150> PRIOR APPLICATION NUMBER: US 60/533,103
27 <151> PRIOR FILING DATE: 2003-12-29
29 <160> NUMBER OF SEQ ID NOS: 17
31 <170> SOFTWARE: PatentIn version 3.2
33 <210> SEQ ID NO: 1
34 <211> LENGTH: 1232
35 <212> TYPE: DNA
36 <213> ORGANISM: Homo sapiens
39 <220> FEATURE:
40 <221> NAME/KEY: CDS
41 <222> LOCATION: (19)..(1044)
43 <400> SEQUENCE: 1
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45           Met Leu Gly Ala Glu Trp Ser Lys Leu Gln Pro
46           1           5           10
48 acg gaa aag cag cgg tac ctg gat gag gcc gag aga gag aag cag cag      99
49 Thr Glu Lys Gln Arg Tyr Leu Asp Glu Ala Glu Arg Glu Lys Gln Gln
50           15           20           25
52 tac atg aag gag ctg cgg gcg tac cag cag tct gaa gcc tat aag atg      147
53 Tyr Met Lys Glu Leu Arg Ala Tyr Gln Gln Ser Glu Ala Tyr Lys Met
54           30           35           40
56 tgc acg gag aag atc cag gag aag aag atc aag aaa gaa gac tcg agc      195
57 Cys Thr Glu Lys Ile Gln Glu Lys Lys Ile Lys Lys Glu Asp Ser Ser
58           45           50           55
60 tct ggg ctc atg aac act ctc ctg aat gga cac aag ggt ggg gac tgc      243
61 Ser Gly Leu Met Asn Thr Leu Leu Asn Gly His Lys Gly Gly Asp Cys

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62	60					65				70				75					
64	gat	ggc	ttc	tcc	acc	ttc	gat	gtt	ccc	atc	ttc	act	gaa	gag	ttc	ttg			291
65	Asp	Gly	Phe	Ser	Thr	Phe	Asp	Val	Pro	Ile	Phe	Thr	Glu	Glu	Phe	Leu			
66						80				85				90					
68	gac	caa	aac	aaa	gcg	cgt	gag	gcg	gag	ctt	cgg	cgc	ttg	cgg	aag	atg			339
69	Asp	Gln	Asn	Lys	Ala	Arg	Glu	Ala	Glu	Leu	Arg	Arg	Leu	Arg	Lys	Met			
70				95					100				105						
72	aat	gtg	gcc	ttc	gag	gag	cag	aac	gcg	gta	ctg	cag	agg	caa	aac	gca			387
73	Asn	Val	Ala	Phe	Glu	Glu	Gln	Asn	Ala	Val	Leu	Gln	Arg	Gln	Asn	Ala			
74			110					115				120							
76	gag	cat	gag	cag	cgc	gcg	cga	gcg	tct	gga	gca	gga	gct	ggc	gct	gga			435
77	Glu	His	Glu	Gln	Arg	Ala	Arg	Ala	Ser	Gly	Ala	Gly	Ala	Gly	Ala	Gly			
78		125					130					135							
80	gga	gcg	gag	gac	gct	ggc	gct	gca	gca	gca	gct	cca	ggc	cgt	gcg	cca			483
81	Gly	Ala	Glu	Asp	Ala	Gly	Ala	Ala	Ala	Ala	Ala	Pro	Gly	Arg	Ala	Pro			
82	140					145				150				155					
84	ggc	gct	cac	cgc	cag	ctt	cgc	ctc	act	gcc	ggg	gcc	ggg	cac	ggg	cga			531
85	Gly	Ala	His	Arg	Gln	Leu	Arg	Leu	Thr	Ala	Gly	Ala	Gly	His	Gly	Arg			
86				160				165				170							
88	aac	gcc	cac	gct	ggg	cac	tct	gga	ctt	cta	cat	ggc	ccg	gct	tca	cgg			579
89	Asn	Ala	His	Ala	Gly	His	Ser	Gly	Leu	Leu	His	Gly	Pro	Ala	Ser	Arg			
90			175					180				185							
92	agc	cat	cga	gcg	cga	ccc	cgc	cca	gca	cga	gaa	gct	cat	cgt	ccg	cat			627
93	Ser	His	Arg	Ala	Arg	Pro	Arg	Pro	Ala	Arg	Glu	Ala	His	Arg	Pro	His			
94			190					195				200							
96	caa	gga	aat	cct	ggc	cca	ggg	cgc	cag	cga	gca	cct	gtg	agg	agt	ggg			675
97	Gln	Gly	Asn	Pro	Gly	Pro	Gly	Arg	Gln	Arg	Ala	Pro	Val	Arg	Ser	Gly			
98		205				210				215									
100	cgg	gcc	cac	gat	gca	gag	gag	aag	ctg	tgg	gcg	cgg	ccc	tgc	cac	acc			723
101	Arg	Ala	His	Asp	Ala	Glu	Lys	Leu	Trp	Ala	Arg	Pro	Cys	His	Thr				
102	220					225				230				235					
104	cca	ccc	cgt	gga	cga	gag	gct	ggg	ggg	cca	ccc	ttt	ggg	gcc	tgg	tcc			771
105	Pro	Pro	Arg	Gly	Arg	Glu	Ala	Gly	Gly	Pro	Pro	Phe	Gly	Ala	Trp	Ser			
106				240				245				250							
108	cat	cct	gca	cct	ttg	ggg	gct	cca	gcc	ccc	cta	aaa	tta	aat	ttc	tgc			819
109	His	Pro	Ala	Pro	Leu	Gly	Ala	Pro	Ala	Pro	Leu	Lys	Leu	Asn	Phe	Cys			
110			255					260				265							
112	agc	atc	cct	tta	gct	ttc	aat	ctc	ccc	agc	ccc	ctg	aac	ccg	gaa	aaa			867
113	Ser	Ile	Pro	Leu	Ala	Phe	Asn	Leu	Pro	Ser	Pro	Leu	Asn	Pro	Glu	Lys			
114			270					275				280							
116	gca	ctc	gct	gcg	cga	tac	acc	cag	aag	aac	ctc	aca	gcc	gag	ggg	gcc			915
117	Ala	Leu	Ala	Ala	Arg	Tyr	Thr	Gln	Lys	Asn	Leu	Thr	Ala	Glu	Gly	Ala			
118		285				290				295									
120	cct	cct	cgg	agg	aca	gcc	acg	cgc	tac	act	ggc	tct	ccg	ggc	cac	ccc			963
121	Pro	Pro	Arg	Arg	Thr	Ala	Thr	Arg	Tyr	Thr	Gly	Ser	Pro	Gly	His	Pro			
122	300					305				310				315					
124	cag	gac	aca	ggg	cag	acg	aaa	ccc	acc	ccc	agc	aca	cgg	cag	gac	ccc			1011
125	Gln	Asp	Thr	Gly	Gln	Thr	Lys	Pro	Thr	Pro	Ser	Thr	Arg	Gln	Asp	Pro			
126				320				325				330							

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128 cca aat tac tca cta cgg ggg gct gtg cca tag gccacacagg aagctgcctt      1064
129 Pro Asn Tyr Ser Leu Arg Gly Ala Val Pro
130          335          340
132 gtggggactt acctggggtg tccccgcacat gcctgtaccc cagatgggtg ggggccggct      1124
134 ttgcccatcc tgctctcctc cagccgaggg accctgggtg ggggtggctcc ttctcactgc      1184
136 tggatccgga ctttttaaataaaaaacaagt aaaatttggtg ttttaaaa      1232
139 <210> SEQ ID NO: 2
140 <211> LENGTH: 341
141 <212> TYPE: PRT
142 <213> ORGANISM: Homo sapiens
144 <400> SEQUENCE: 2
146 Met Leu Gly Ala Glu Trp Ser Lys Leu Gln Pro Thr Glu Lys Gln Arg
147 1          5          10          15
150 Tyr Leu Asp Glu Ala Glu Arg Glu Lys Gln Gln Tyr Met Lys Glu Leu
151          20          25          30
154 Arg Ala Tyr Gln Gln Ser Glu Ala Tyr Lys Met Cys Thr Glu Lys Ile
155          35          40          45
158 Gln Glu Lys Lys Ile Lys Lys Glu Asp Ser Ser Ser Gly Leu Met Asn
159          50          55          60
162 Thr Leu Leu Asn Gly His Lys Gly Gly Asp Cys Asp Gly Phe Ser Thr
163 65          70          75          80
166 Phe Asp Val Pro Ile Phe Thr Glu Glu Phe Leu Asp Gln Asn Lys Ala
167          85          90          95
170 Arg Glu Ala Glu Leu Arg Arg Leu Arg Lys Met Asn Val Ala Phe Glu
171          100         105         110
174 Glu Gln Asn Ala Val Leu Gln Arg Gln Asn Ala Glu His Glu Gln Arg
175          115         120         125
178 Ala Arg Ala Ser Gly Ala Gly Ala Gly Ala Gly Glu Ala Glu Asp Ala
179          130         135         140
182 Gly Ala Ala Ala Ala Ala Pro Gly Arg Ala Pro Gly Ala His Arg Gln
183 145         150         155         160
186 Leu Arg Leu Thr Ala Gly Ala Gly His Gly Arg Asn Ala His Ala Gly
187          165         170         175
190 His Ser Gly Leu Leu His Gly Pro Ala Ser Arg Ser His Arg Ala Arg
191          180         185         190
194 Pro Arg Pro Ala Arg Glu Ala His Arg Pro His Gln Gly Asn Pro Gly
195          195         200         205
198 Pro Gly Arg Gln Arg Ala Pro Val Arg Ser Gly Arg Ala His Asp Ala
199          210         215         220
202 Glu Glu Lys Leu Trp Ala Arg Pro Cys His Thr Pro Pro Arg Gly Arg
203 225         230         235         240
206 Glu Ala Gly Gly Pro Pro Phe Gly Ala Trp Ser His Pro Ala Pro Leu
207          245         250         255
210 Gly Ala Pro Ala Pro Leu Lys Leu Asn Phe Cys Ser Ile Pro Leu Ala
211          260         265         270
214 Phe Asn Leu Pro Ser Pro Leu Asn Pro Glu Lys Ala Leu Ala Ala Arg
215          275         280         285
218 Tyr Thr Gln Lys Asn Leu Thr Ala Glu Gly Ala Pro Pro Arg Arg Thr
219          290         295         300

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222 Ala Thr Arg Tyr Thr Gly Ser Pro Gly His Pro Gln Asp Thr Gly Gln
223 305                               310                               315                               320
226 Thr Lys Pro Thr Pro Ser Thr Arg Gln Asp Pro Pro Asn Tyr Ser Leu
227                               325                               330                               335
230 Arg Gly Ala Val Pro
231                               340
234 <210> SEQ ID NO: 3
235 <211> LENGTH: 3870
236 <212> TYPE: DNA
237 <213> ORGANISM: Homo sapiens
240 <220> FEATURE:
241 <221> NAME/KEY: CDS
242 <222> LOCATION: (179)..(1642)
244 <400> SEQUENCE: 3
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247 aaaagttttt cttgtggaac aagttaacac tagatggcag ataacagact gaggagtgag      120
249 ctgcttctga ctcgattaaa aagggagtga gccataactg gcggctgctc ttctcgcca      178
251 atg agc ctc ccc aat tcc tcc tgc ctc tta gaa gac aag atg tgt gag      226
252 Met Ser Leu Pro Asn Ser Ser Cys Leu Leu Glu Asp Lys Met Cys Glu
253 1                               5                               10                               15
255 ggc aac aag acc act atg gcc agc ccc cag ctg atg ccc ctg gtg gtg      274
256 Gly Asn Lys Thr Thr Met Ala Ser Pro Gln Leu Met Pro Leu Val Val
257                               20                               25                               30
259 gtc ctg agc act atc tgc ttg gtc aca gta ggg ctc aac ctg ctg gtg      322
260 Val Leu Ser Thr Ile Cys Leu Val Thr Val Gly Leu Asn Leu Leu Val
261                               35                               40                               45
263 ctg tat gcc gta cgg agt gag cgg aag ctc cac act gtg ggg aac ctg      370
264 Leu Tyr Ala Val Arg Ser Glu Arg Lys Leu His Thr Val Gly Asn Leu
265                               50                               55                               60
267 tac atc gtc agc ctc tcg gtg gcg gac ttg atc gtg ggt gcc gtc gtc      418
268 Tyr Ile Val Ser Leu Ser Val Ala Asp Leu Ile Val Gly Ala Val Val
269 65                               70                               75                               80
271 atg cct atg aac atc ctc tac ctg ctc atg tcc aag tgg tca ctg ggc      466
272 Met Pro Met Asn Ile Leu Tyr Leu Leu Met Ser Lys Trp Ser Leu Gly
273                               85                               90                               95
275 cgt cct ctc tgc ctc ttt tgg ctt tcc atg gac tat gtg gcc agc aca      514
276 Arg Pro Leu Cys Leu Phe Trp Leu Ser Met Asp Tyr Val Ala Ser Thr
277                               100                              105                              110
279 gcg tcc att ttc agt gtc ttc atc ctg tgc att gat cgc tac cgc tct      562
280 Ala Ser Ile Phe Ser Val Phe Ile Leu Cys Ile Asp Arg Tyr Arg Ser
281                               115                              120                              125
283 gtc cag cag ccc ctc agg tac ctt aag tat cgt acc aag acc cga gcc      610
284 Val Gln Gln Pro Leu Arg Tyr Leu Lys Tyr Arg Thr Lys Thr Arg Ala
285                               130                              135                              140
287 tcg gcc acc att ctg ggg gcc tgg ttt ctc tct ttt ctg tgg gtt att      658
288 Ser Ala Thr Ile Leu Gly Ala Trp Phe Leu Ser Phe Leu Trp Val Ile
289 145                              150                              155                              160
291 ccc att cta ggc tgg aat cac ttc atg cag cag acc tcg gtg cgc cga      706
292 Pro Ile Leu Gly Trp Asn His Phe Met Gln Gln Thr Ser Val Arg Arg

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293		165		170		175		
295	gag	gac	aag	tgt	gag	aca	gac	ttc
296	Glu	Asp	Lys	Cys	Glu	Thr	Asp	Phe
297				180				185
299	atg	act	gcc	atc	atc	aac	ttc	tac
300	Met	Thr	Ala	Ile	Ile	Asn	Phe	Tyr
301			195				200	
303	ttc	tat	gcc	aag	atc	tac	aag	gcc
304	Phe	Tyr	Ala	Lys	Ile	Tyr	Lys	Ala
305		210				215		220
307	gag	ctc	atc	aat	agg	tcc	ctc	cct
308	Glu	Leu	Ile	Asn	Arg	Ser	Leu	Pro
309	225				230			235
311	cca	gag	aac	ccc	aag	ggg	gat	gcc
312	Pro	Glu	Asn	Pro	Lys	Gly	Asp	Ala
313				245				250
315	tgg	gag	gtt	ctg	aaa	agg	aag	cca
316	Trp	Glu	Val	Leu	Lys	Arg	Lys	Pro
317			260				265	
319	ttg	aag	tca	cca	tcc	caa	acc	ccc
320	Leu	Lys	Ser	Pro	Ser	Gln	Thr	Pro
321			275				280	
323	ttc	agc	caa	gag	gat	gat	aga	gaa
324	Phe	Ser	Gln	Glu	Asp	Asp	Arg	Glu
325		290				295		300
327	ctt	gat	att	gtg	cac	atg	cag	gct
328	Leu	Asp	Ile	Val	His	Met	Gln	Ala
329	305					310		315
331	tat	gta	gcc	gtc	aac	cgg	agc	cat
332	Tyr	Val	Ala	Val	Asn	Arg	Ser	His
333				325				330
335	ggc	ctg	aac	aca	cat	ggg	gcc	agc
336	Gly	Leu	Asn	Thr	His	Gly	Ala	Ser
337			340				345	
339	ggt	gat	agc	caa	tcc	ttc	tct	cga
340	Gly	Asp	Ser	Gln	Ser	Phe	Ser	Arg
341		355					360	
343	aca	gca	cca	ggc	aaa	ggc	aaa	ttg
344	Thr	Ala	Pro	Gly	Lys	Gly	Lys	Leu
345		370				375		380
347	gat	tac	atc	aag	ttt	act	tgg	aag
348	Asp	Tyr	Ile	Lys	Phe	Thr	Trp	Lys
349	385				390			395
351	tat	gta	tct	ggg	ttg	cac	atg	aac
352	Tyr	Val	Ser	Gly	Leu	His	Met	Asn
353				405				410
355	ttg	ggt	ttt	atc	atg	gca	gcc	ttc
356	Leu	Gly	Phe	Ile	Met	Ala	Ala	Phe
357			420				425	
								430

**VERIFICATION SUMMARY**

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Input Set : A:\sequence listing.txt

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L:17 M:270 C: Current Application Number differs, Wrong Format

L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date